

GenCore version 5.1.4-p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:16:08 ; Search time 4401.47 Seconds

(without alignments)  
10982.631 Million cell updates/sec

Title: US-09-001-737-7

Perfect score: 1661

Sequence: 1 GATTTCGGCTTCATATGCA.....TGGCGGATTAAGCCGATTC 1661

Scoring table: IDENTIFY\_MUC

Gapop 10.0 ; Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank  
1: gb\_ba:\*  
2: gb\_hg:\*  
3: gb\_in:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_ov:\*  
7: gb\_ov:\*  
8: gb\_ov:\*  
9: gb\_ov:\*  
10: gb\_ov:\*  
11: gb\_ov:\*  
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40: gb\_ov:\*  
41: gb\_ov:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1622.2	97.7	10389	AE006627	AE006627 Streptococcus
2	1607.8	96.8	53291	AE014170	AE014170 Streptococcus
3	1604.6	96.6	11576	AE010115	AE010115 Streptococcus
4	1413.4	85.1	2683	SPK0610N	X89236 S. pyogenes
5	1413.4	85.1	2683	AX148805	AX148805 Sequence
6	1170.4	70.5	1421	AX121365	AX121365 Streptococcus
7	1140.4	68.7	1306	AX148806	AX148806 Sequence
8	1128.8	68.0	1421	AX121364	AX121364 Streptococcus
9	1125	67.7	1422	AX121366	AX121366 Streptococcus
10	1122.6	67.6	1305	AX148809	AX148809 Sequence
11	1118	67.3	1415	AX121367	AX121367 Streptococcus
12	1104.2	66.5	2054	AF389514	AF389514 Streptococcus
13	1080	65.0	1384	AX121363	AX121363 Streptococcus
14	1076.4	64.8	2324	AF389516	AF389516 Streptococcus
15	1068.6	64.3	2320	AF389515	AF389515 Streptococcus
16	1064.6	64.1	2020	AF389517	AF389517 Streptococcus
17	1053.8	63.4	1718	AF389517	AF389517 Streptococcus
18	1050.8	63.3	2639	AF378195	AF378195 Streptococcus
19	1050.8	63.3	2750	AF378196	AF378196 Streptococcus
20	1039.2	62.6	1653	AX194119	AX194119 Sequence
21	1038.6	62.5	21454	SPK0610N	AX194119 Sequence
22	1038.6	62.5	1926	AX073958	AX073958 Streptococcus
23	1037	62.4	2107	AF325449	AF325449 Streptococcus
24	1037	62.4	2107	AX148804	AX148804 Sequence
25	1036	62.4	1647	AX194338	AX194338 Streptococcus
26	1035.4	62.3	5365	BD003757	BD003757 Polynucleotide
27	1035.4	62.3	11318	AE008538	AE008538 Streptococcus
28	1035.4	62.3	13103	AE007482	AE007482 Streptococcus
29	1030.6	62.0	2401	AF117741	AF117741 Streptococcus
30	1030.6	62.0	2401	AX148803	AX148803 Sequence
31	1014	61.0	3666	AF338228	AF338228 Streptococcus
32	1013.2	61.0	1963	AY038047	AY038047 Streptococcus
33	1013.2	61.0	2490	AF378197	AF378197 Streptococcus
34	955	57.5	12560	AE006276	AE006276 Streptococcus
35	948.6	57.1	2267	AF389517	AF389517 Streptococcus
36	942.2	56.7	2187	AY029215	AY029215 Streptococcus
37	942	56.7	3120	AF335185	AF335185 Streptococcus
38	840.4	50.8	2853	AB073399	AB073399 Streptococcus
39	840.4	50.6	2834	AB028452	AB028452 Streptococcus
40	838.8	50.5	2309	1	1
41	832	50.1	1901	AX148805	AX148805 Sequence
42	824	49.6	213251	AX141015	AX141015 Sequence
43	824	49.6	349980	AX141015	AX141015 Sequence
44	822.4	49.5	2156	AF335322	AF335322 Streptococcus
45	822.4	49.5	295050	AL591982	AL591982 Streptococcus

## ALIGNMENTS

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LOCUS  
DEFINITION  
Streptococcus pyogenes M1 GAS strain SF370, section 156 of 167 of the complete genome.  
ACCESSION  
AE006627 AE004092  
VERSION  
AE006627.1 GI:13623059  
KEYWORDS  
SOURCE  
ORGANISM  
Streptococcus pyogenes M1 GAS.  
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus  
1 (bases 1 to 10389)  
REFERENCE  
AUTHORS  
Ferretti J.J., McShan M.M., Adjuic D., Savic D., Lyon K., Primeaux C., Szabo S.S., Sidorov A.N., Kenton S., Lal H., Lin S.,



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DB	4794	CGCTTCAAAATGACCTCTGTGATGAGTCTTATTTGAACAAAGAGTGTGCTA	4735
OY	1573	ATAAAGCTGAACAGCTACGCGCAGCCGCAAGATGCGAGAGATGATGCAAGAT	1632
DB	4734	ATAAAGCTGAACAGCTACGCGCAGCCGCAAGATGCGAGAGATGATGCAAGAT	4675
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DB	4674	TGGGTGG 4668	

AE014170/c 53291 bp DNA linear BCT 19-JUL-2002  
LOCUS Streptococcus pyogenes MGAS315, section 35 of 37 of the complete  
DEFINITION genome.  
ACCESSION AE014170 AE014074  
VERSION AE014170.1 GI:21905475  
KEYWORDS  
SOURCE  
ORGANISM Streptococcus pyogenes MGAS315.  
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
Streptococcus.  
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Beres, S.B., Sylva, G.L., Barbican, K.D., Lei, B., Hoff, J.S.,  
Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F.,  
Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and  
Musser, J.M.  
TITLE Genome sequence of a serotype M3 strain of group A Streptococcus:  
Phage-encoded toxins, the high-virulence phenotype, and clone  
emergence  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)  
REFERENCE 2 (bases 1 to 53291)  
Beres, S.B., Sylva, G.L., Barbican, K.D., Lei, B., Hoff, J.S.,  
Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F.,  
Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and  
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TITLE Submitted (14-JUN-2002) Laboratory of Human Bacterial Pathogenesis,  
JOURNAL Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,  
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REFERENCE  
 AUTHORS Smoot J.C., Barblian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang O., Kapur V., Daly J.A., Veasy L.G. and Musser J.M.  
 TITLE genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002)  
 MEDLINE 21927593  
 PUBMED 11917108

REFERENCE  
 AUTHORS Smoot J.C., Barblian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang O., Kapur V., Daly J.A., Veasy L.G. and Musser J.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-JAN-2002) Laboratory of Human Bacterial Pathogenesis/Rocky Mountain Laboratories/NIH/NIH, 903 S. 4th St., Hamilton, MT 59840, USA

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 VERSION AY121365.1 GI:22022489  
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 ORGANISM Streptococcus dysgalactiae subsp. equisimilis.  
 Streptococcus dysgalactiae subsp. equisimilis.  
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 Streptococcus.  
 REFERENCE 1 (bases 1 to 1421)  
 AUTHORS Woo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. W.,  
 Tse, H., Wong, K. L., Li, K. W., Lam, K. C. and Yuen, K. Y.  
 TITLE Streptococcus dysgalactiae subsp. equisimilis  
 JOURNAL Published  
 2 (bases 1 to 1421)  
 DIRECT SUBMISSION  
 Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,  
 Pokfulam Road, Hong Kong, China  
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LOCUS AX148806  
DEFINITION Sequence 8 from Patent WO0136625.  
ACCESSION AX148806  
VERSION AX148806.1 GI:14347330  
KEYWORDS  
SOURCE Streptococcus pyogenes.  
ORGANISM Streptococcus pyogenes  
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
Streptococcus.  
REFERENCE 1 (bases 1 to 1306)  
AUTHORS Wright, J.A., Young, A.H. and Dugourd, P.  
TITLE Antisense oligonucleotide sequences derived from groE1 and groES as  
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Patent: WO 0136625-A 8 25-MAY-2001;  
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 LOCUS chaperonin GroEL gene, partial cds.  
 DEFINITION chaperonin GroEL gene, partial cds.  
 ACCESSION AY121364  
 VERSION AY121364  
 KEYWORDS  
 SOURCE Streptococcus dysgalactiae subsp. equisimilis.  
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

REFERENCE 1 (bases 1 to 1421)  
 AUTHORS Moo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. W., Tse, H., Wong, K. L., Li, K. -W., Lam, K. -C. and Yuen, K. -Y.  
 TITLE Chaperonin GroEL gene of Group C Streptococcus dysgalactiae subsp. equisimilis  
 JOURNAL Unpublished  
 AUTHORS Moo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. -W., Tse, H., Wong, K. L., Li, K. -W., Lam, K. -C. and Yuen, K. -Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-JUN-2002) Microbiology, The University of Hong Kong, Pokfulam Road, Hong Kong, China

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 LOCUS AX148809  
 DEFINITION Sequence 11 from Patent WO0136625.  
 ACCESSION AX148809  
 VERSION AX148809.1 GI:14347333  
 KEYWORDS  
 SOURCE Streptococcus pyogenes.  
 ORGANISM Streptococcus pyogenes.  
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 Streptococcus.  
 REFERENCE  
 AUTHORS Wright, J.A., Young, A.H. and Dugourd, D.  
 TITLE Antisense oligonucleotide sequences derived from groEL and groES as  
 inhibitors of microorganisms  
 JOURNAL Patent: WO 0136625-A 11 25-MAY-2001.  
 FEATURES  
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 Location/Qualifiers  
 BASE COUNT 406 a 238 c 312 g 349 t  
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 Query Match 67.6%, Score 1122.6, DB 6, Length 1305;  
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 VERSION AY121367.1 GI:22022493  
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 Streptococcus.  
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 AUTHORS Moo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,  
 Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.  
 TITLE Chapteronin GroEL gene of Group G Streptococcus dysgalactiae  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1415)  
 AUTHORS Moo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,  
 Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,  
 Pokfulam Road, Hong Kong, China  
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**SOURCE** Streptococcus bovis.  
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**REFERENCE** 1 (bases 1 to 2054)  
**AUTHORS** Teng, L.-J.  
**TITLE** The groEL genes of Streptococcus bovis  
**JOURNAL** unpublished  
**REFERENCE** 2 (bases 1 to 2054)  
**AUTHORS** Teng, L.-J.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (08-JUN-2001) School of Medical Technology, National  
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Wed Apr 16 08:05:36 2003

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ORGANISM Streptococcus dysgalactiae subsp. dysgalactiae  
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AUTHORS Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,  
Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.  
TITLE Chapter 11 GroEL, gene of Group C Streptococcus dysgalactiae  
subspecies dysgalactiae  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1384)  
AUTHORS Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,  
Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.  
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DB 961 GTTGTGACTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
OY 1138 CTGTTATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197  
DB 1021 CTGTTATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080  
OY 1198 AGCATGCTTAAATGCTACAGGCTGATGATGATGATGATGATGATGATGATGATG 1257  
DB 1081 AAGCATGCTTAAATGCTACAGGCTGATGATGATGATGATGATGATGATGATGATG 1140  
OY 1258 CAGCATTTATAGGCTTATGAAAGATGATGATGATGATGATGATGATGATGATG 1317  
DB 1141 CAGCATTTATAGGCTTATGAAAGATGATGATGATGATGATGATGATGATGATG 1200  
OY 1318 CTGAGCTTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1377  
DB 1201 CTGAGCTTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
OY 1378 CTGAGCTTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1437  
DB 1261 CTGAGCTTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
OY 1438 TTAATGCTGCAAGAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATG 1497  
DB 1321 TTAATGCTGCAAGAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATG 1380  
OY 1498 AAGT 1501  
DB 1381 AAGT 1384  
RESULT 14  
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D	956	TATGATATTGGCCGGTACATGGGACACAGACAGCAGCTGTGTAACTCAGAGCTATTGTCC	1015
OY	314	TCAGAGCTAAAAATTGTGACAGCAGGCTCTATTCATTTGGTATCCGTGAGGCAATGA	373
D	1016	TCAGAGCTTTAAAAATTGTGACTGTGACACTTACCCCAATGGATATTCGTTCAGAGAAATCA	1075
OY	374	AACAGCAACGACACAGCTGTTGAGCCTTGAAGCCATTGCTCAACCTGTATCTGGCA	433
D	1076	AACACACAGTTGCACACAGCAGTTGTAGATTGAAGCTATTGACACAGCCTGTTCTTGGCA	1135
OY	434	GGAGACTATTGTCAGAGCTGGCTGACGTATCATCAGCAGCTCGAAGAAAGTTGGAGAGTAT	493
D	1136	AGAGAGCTATTGTCAGAGCTGGCTGACAGCTTTATCATCAGCTTCGAAAAAGTTGGGCAATACGT	1195
OY	494	CTCAGAGCTATGAGAGCCTGGGGCAACAGTATGTATACCATTCAGAGAAATCTGAG	553
D	1196	TTCTGAGCATATGAAAAAGTTGGTAAACATGTGTATTACATATTGAAGAACTCGTG	1255
OY	554	TATGAAACAGAACTTGAAGTGGTGAAGGATGCATTTGACGCGTGTATCCGTCTCA	613
D	1256	TATGAAACAGAACTTGAAGTGGTGAAGGATGCATTTGATCCGCGCTACCTTTCCA	1315
OY	614	ATATCTGGTACAGACATGAAAAATGGTTGGACGCTTGAAGAACCATTTATCTAT	673
D	1316	ATATTTGGTATACGACATGAAAAATGGTGGCAGACTTGAAGAACTTTATTGTTAT	1375
OY	674	CAGGATAAAAAGTGTAAACATTCAGACACTTTCCCACTTGTGAGAACTTTAA	733
D	1376	TCAGATTAATAAATTTCAAAATTCACAAATGTCTTCGCTCTTCAAGAAAGTCTTAA	1435
OY	734	AACCAACCTTCCATTACATTTATTCAGATGATGTGATGGTGAAGCACTTCCAACTT	793
D	1436	GACACACGCTCTCTTTTAATATTCGGAATGATGATGATGAGAGCTCTCCAAAGCT	1495
OY	794	TGCTCTTAACAGATCTGTGACTTTCATATGTGGTGTGCTCAAGCCGACAGATTTGG	853
D	1496	TGTTTTCATTAAGATCTGTGACTTTCATTAAGTGTGCTCAAGCTCTCTGTTTGG	1555
OY	854	TGATCTGCTGAAGCTATGCTTGAAGACATGCTATCTTGACAGGTGGTACAGTATTA	913
D	1556	TGATCTGCTGAAGGCACTGCTGAAGATATTTGCTGTTTAAAGGGGGTACTGTTTAA	1615
OY	914	AGAGAGCTTAGAGACTTGAATTTAAAGATCTTACAAATACAGCCCTTGGACAGGCTCTAA	973
D	1616	TGAAGATCTTGGCTCTAGATTTGAAGATACAGCATTTGATAGCTTGGGTCAACGACCTG	1675
OY	974	GATTACAGTTGAATTAAGATATGACACAGTATTTGTTGAAGGTAGAGAAATTCAGAACTAT	1033
D	1676	TGTGACAGTTGAATTAAGATATGACACAGTATTTGTTGAAGGTAGAGAACTAT	1735
OY	1034	TGCTACACCGATATGACAGTATTAATCCGATTTGAAGACAAACATTTGACTTGAAGC	1093
D	1736	TGCTACACCGTATCATCTCAATTAAGTCTCAATTTGAAGCAACCACTTCAAGCTTTGATG	1795
OY	1094	TGAAGAACTTCAAGAAAGCTTTGGCGAAATTAAGCTGTGTGATGCTGTATCAAAATGAG	1153
D	1796	TGAAGAACTTCAAGAAAGCTTTGGCTAAATTAATCTGGAAGGTGTGGCGTCAATCAAGTGG	1855
OY	1154	AGCTTCAAGAGAGAGCTTTAAAGAAATGAACCTTCGATTTGAGATGCTCTAAATGC	1213
D	1856	CGCAGACACAGAAAGAAATTTGAAGAAATTAACAACTTCGATTTGAAGATGCGCTTAAATGC	1915
OY	1214	TACACGTGACGCCGTTGAAGAGATATCGTGTGCTGGTGGTGAACAGCACTTTATACGT	1273
D	1916	TACTGAGCAGCGCTGTGAAGAGAAATTTGTGTGACAGGTGGTGAAGAGCGCACTTCAAACT	1975
OY	1274	TATTGAAAGATGACAGCTGTGTGAGCTTTGAAGGCGATGATGCTACTGAGAGCTAACTGT	1333
D	1976	TATTGAAAGATGACAGCTGTGTGAGCTTTTAATTAACAGATGCTGTGCAACAGGTGCAACTTGT	2035
OY	1334	GCTTGTGCTCTAGAAAGGCTCTAGCTCAAAATGCTTTAAATGCTGTGGTACAGAGCTC	1393
D	2036	TCCTGCTGCTCTTGAAGAGGCTCTCGCTCAAAATGCTTTAAATGCTGTGGTATGAAAGCTC	2095

	Accession	1537	Conservative	0	Mismatches	314	Indels	0	Gaps
QY	13	ATATGCGAAAGAAATCAATTTTGCAGCAGATGGCGGTGCTGCGCATGTGTCGGAGATTG	72						
Db	717	AAATGGCAAAAGATTAATTAATTTTCACGAGATGAAGAAGTGCATAGTACGTGGTGTGC	776						
QY	73	ATATGTTACAGATACCGTCAAGATACGCGATGTCTAAAGGGCGCAATGTTGTTCTG	1322						
Db	777	ATATTTTACAGATACCGTTAAAGTAATCTAGAGACCTAAAGGACGAATGTTGTTCTTG	826						
QY	133	AAAACGTTTGGTTCCTCCCTTAATTTACTATACGGGGTAACCATGTGCTAAAGATCG	192						
Db	837	AGAAATCATTTGGGTCAACCGCTCATCACAATGACGGTGTGCTATTTGCCAAAGAAATG	896						
QY	193	AATTAAAGATCATTTTGAAGAACGSSGCAAAATTTGTTCTGAAAGGCTGTAAA	232						
Db	897	AACGCAAGATCATTTTGAAGAAATATGGGCCCTAAGTGGTGTCAAGATTGCTTAAGAA	956						
QY	253	CGAATATATTTGCTGGTGGATGGGACGACTACTGCAAGCTTTTACACAGCATTTGTC	312						
Db	957	CTATATATATGCTGGTGGACGGCAACACTACTGCGACTGTCTTACCCCAAGCATGTGC	101						
QY	313	ATCAAGGACTAAAAATGTGTACAGCAGGTCTATCAATTTGTTATCCGTGAGGCATTG	372						
Db	1017	GCGAAGGATCAAAAATGTATACGGCTGTGTCAAAACCAATTTGGCATCTCTGTGTATTG	107						
QY	373	AAACGACAACGCAACGCTGTTTGAAGCTTGAAGCCATGTCTCAACCTGATGTGCA	432						
Db	1077	AAACGACCTGTGCAACGCTGTGAAGCTTTAAAGCAAAATTCGTGTCCAGTTTCTATA	1133						
QY	433	AGGAAGCTATTGTCACAGTCTGCTGAGATCATCAAGCTCTGAAGAAATGTGAGAGATA	492						
Db	1137	AACAGACCATTTGCAACAGTTGCTGTCTCATCAAGCTTGTGAAAAAGTGGAGAAATCA	1199						
QY	493	TCGCAAGAGCTATGAGCGCTGTGGGGCAAGATGGTGTATTACATCTGCAAGAAATCTGAG	552						
Db	1197	TCGTCGAAGCCATGAAAAAGTTGTGGCAACGCGTGTATCATCATTTGAAGATCAAAAG	1255						
QY	553	GTTATGGAACGAACTTGAAGTGTGTGAAGGCATGCAATTTGACCTGGTTACCTGTCTC	612						
Db	1257	GATGCAACAGACCTAGTATGTTGTAAAGTATGAGTTGACCGTGGCTATCTCTTCTC	1311						
QY	613	AATACATGCTCACAGCAATGAAAAATGTTGTCAGACCTGAAAAACCATTTATCTTAA	672						
Db	1317	AATACATGTATACAGCAATGAAAAATGTTGTCGATTGTGATATCCATATATCTTTGA	1376						
QY	673	TCACGATTAAAAAAGTCCAAACATCCCAAGACATTTTCCACACTTGTGAGACCTTTTA	732						
Db	1377	TTACAGATTAAGAGATTTCATATATCCCAAAATCTTCTTTGTTGGAAAAATTTTAA	1436						
QY	733	AAACCAACCGTCACTTACATCATTTATTCACAGATATGGAATGGTGAAGCACTGTCCAAACG	792						
Db	1437	AAACAGTGTGCGGCTTTGATTTATTCACAGATATGGAATGGTGAAGCTCTTCCAAATC	1496						
QY	793	TTGTTTSAACAGATATGCTGTCTTCTTCAATGTGTTGCTGTCAACAGCCGAGATTGG	852						
Db	1497	TTGTTTSAACAAATTCGTTGTATCTTCAATGATGCTGTGGAAGAGCGCAAGGATTGG	1556						
QY	853	GTGATCGTCTGAAGCTATGCTTGAAGCATGTGCTATCTTGGACAGGTGTACAGTATTA	912						
Db	1557	GTGACCGGTGAAGGGGATGCTGAAGATATTTGCCATTTTGGATGTGGCGGTCAAGTATTA	1616						
QY	913	CAGAGATCTAGCACTTAATTAAGATGCTACAAATGAAGCCCTGGAGAGGCTGTCA	972						
Db	1617	CAGAAAGATCTTGTGTGTAATTTGAAGATGCAACCATTTGAAGCACTGTGACAGGCTCA	1676						
QY	973	AGATTACAGTTGATTAAGATAGCAGATATGTGAAGGTTTCAAGAGTTCCAGAAGCTA	1032						
Db	1677	AGTTAAGTGTGATTAAGACAGCACGCTTATGTGTGAAGGCTGTGATGCTGAAGCA	1736						
QY	1033	TTGCTAACCTATGCACTGATTAATATGCCATTTGAAGAACCAACTTGTGACTTTGAC	1092						
Db	1737	TTGCTAACCGCGTGTGTCTTAATATGCAAAATTTGAATGCTATCAATCTTAATTTTGA	1786						

